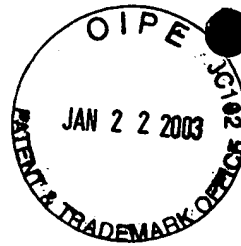


SEQUENCE LISTING



#12/B

<110> CLAUSEN, Henrik

<120> UDP-N-ACETYLGLUCOSAMINE: GALACTOSE-B1, 3-N-ACETYLGLACTOSAMINE-a-R / N-ACETYL GLUCOSAMINE-B1,3-N-ACETYLGLACTOSAMINE-a-R (GlcNAc to GalNAc) B1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE, C2/4GnT

<130> 4305/0J425

<140> US 09/874,390

<141> 2001-06-04

<150> DK PA 1988 01605

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| ttgttctggg aagccctggg attctgctaa tacctatcac tgtaggtgct gaagggaaac | 180 |
| agatgaagaa catgacctca aggagcttcc tgtcaatgag aagaccaagc tgacgcctgg | 240 |
| caaagatatt aaagaggagc ctgaaactgt tccttgagaca tcttatgaat gtcagaaaat | 300 |
| accttttgga gggtagaag atcaggggac atgggtgttc acatttgctg ccacggaaca | 360 |
| ccgccagtct tcacttgga acagaatcac gccttgtaga gagatcatcc ctaagcagga | 420 |
| gagaagctac taaaggattg tgcctcctc caccttccct gtgctcggtc tccacctgct | 480 |
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| Met Val Gln Trp Lys Arg Leu Cys Gln Leu His Tyr | |
| 1 5 10 | |
| ttg tgg gct ctg ggc tgc tat atg ctg ctg gcc act gtg gct ctg aaa | 579 |
| Leu Trp Ala Leu Gly Cys Tyr Met Leu Leu Ala Thr Val Ala Leu Lys | |
| 15 20 25 | |
| ctt tct ttc agg ttg aag tgt gac tct gac cac ttg ggt ctg gag tcc | 627 |
| Leu Ser Phe Arg Leu Lys Cys Asp Ser Asp His Leu Gly Leu Glu Ser | |

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| agg gaa tct caa agc cag tac tgt agg aat atc ttg tat aat ttc ctg Arg Glu Ser Gln Ser Gln Tyr Cys Arg Asn Ile Leu Tyr Asn Phe Leu 45 50 55 60 | | | 675 |
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| agc aaa gaa gag gtg gag ttc cct att gca tac tct atg gtg att cat Ser Lys Glu Glu Val Glu Phe Pro Ile Ala Tyr Ser Met Val Ile His 125 130 135 140 | | | 915 |
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| cag aac ata tac tgt gtc cat gtg gat gag aag tcc cca gaa act ttc Gln Asn Ile Tyr Cys Val His Val Asp Glu Lys Ser Pro Glu Thr Phe 160 165 170 | | | 1011 |
| aaa gag gcg gtc aaa gca att att tct tgc ttc cca aat gtc ttc ata Lys Glu Ala Val Lys Ala Ile Ile Ser Cys Phe Pro Asn Val Phe Ile 175 180 185 | | | 1059 |
| gcc agt aag ctg gtt cgg gtg gtt tat gcc tcc tgg tcc agg gtg caa Ala Ser Lys Leu Val Arg Val Val Tyr Ala Ser Trp Ser Arg Val Gln 190 195 200 | | | 1107 |
| gct gac ctc aac tgc atg gaa gac ttg ctc cag agc tca gtg ccg tgg Ala Asp Leu Asn Cys Met Glu Asp Leu Leu Gln Ser Ser Val Pro Trp 205 210 215 220 | | | 1155 |
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| gca gag atg gtc cag gct ctc aag atg ttg aat ggg agg aat agc atg Ala Glu Met Val Gln Ala Leu Lys Met Leu Asn Gly Arg Asn Ser Met 240 245 250 | | | 1251 |
| gag tca gag gta cct cct aag cac aaa gaa acc cgc tgg aaa tat cac Glu Ser Glu Val Pro Pro Lys His Lys Glu Thr Arg Trp Lys Tyr His 255 260 265 | | | 1299 |

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| ttt gag gta gtg aga gac aca tta cac cta acc aac aag aag aag gat Phe Glu Val Val Arg Asp Thr Leu His Leu Thr Asn Lys Lys Lys Asp 270 275 280 | 1347 |
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| caa ctg att gaa tgg gta aaa gac act tat agc cca gat gaa cac ctg Gln Leu Ile Glu Trp Val Lys Asp Thr Tyr Ser Pro Asp Glu His Leu 320 325 330 | 1491 |
| tgg gcc acc ctt cag cgt gca cgg tgg atg cct ggc tct gtt ccc aac Trp Ala Thr Leu Gln Arg Ala Arg Trp Met Pro Gly Ser Val Pro Asn 335 340 345 | 1539 |
| cac ccc aag tac gac atc tca gac atg act tct att gcc agg ctg gtc His Pro Lys Tyr Asp Ile Ser Asp Met Thr Ser Ile Ala Arg Leu Val 350 355 360 | 1587 |
| aag tgg cag ggt cat gag gga gac atc gat aag ggt gct cct tat gct Lys Trp Gln Gly His Glu Gly Asp Ile Asp Lys Gly Ala Pro Tyr Ala 365 370 375 380 | 1635 |
| ccc tgc tct gga atc cac cag cgg gct atc tgc gtt tat ggg gct ggg Pro Cys Ser Gly Ile His Gln Arg Ala Ile Cys Val Tyr Gly Ala Gly 385 390 395 | 1683 |
| gac ttg aat tgg atg ctt caa aac cat cac ctg ttg gcc aac aag ttt Asp Leu Asn Trp Met Leu Gln Asn His His Leu Leu Ala Asn Lys Phe 400 405 410 | 1731 |
| gac cca aag gta gat gat aat gct ctt cag tgc tta gaa gaa tac cta Asp Pro Lys Val Asp Asp Asn Ala Leu Gln Cys Leu Glu Glu Tyr Leu 415 420 425 | 1779 |
| cgt tat aag gcc atc tat ggg act gaa ctt tgagacacac tatgagagcg Arg Tyr Lys Ala Ile Tyr Gly Thr Glu Leu 430 435 | 1829 |
| ttgctacctg tggggcaaga gcatgtacaa acatgctcag aacttgctgg gacagtgtgg | 1889 |
| gtgggagacc agggctttgc aattcgtggc atcctttagg ataagagggc tgctattaga | 1949 |
| ttgtgggtaa gtagatcttt tgccttgcaa attgctgcct gggatgaatgc tgcttgttct | 2009 |
| ctcacccta accctagtag ttcctccact aactttctca ctaagtgaga atgagaactg | 2069 |
| ctgtgatagg gagagtgaag gagggatatg tggtagagca cttgatttca gttgaatgcc | 2129 |
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Leu Lys Cys Asp Ser Asp His Leu Gly Leu Glu Ser Arg Glu Ser Gln
 35 40 45

Ser Gln Tyr Cys Arg Asn Ile Leu Tyr Asn Phe Leu Lys Leu Pro Ala
 50 55 60

Lys Arg Ser Ile Asn Cys Ser Gly Val Thr Arg Gly Asp Gln Glu Ala
 65 70 75 80

Val Leu Gln Ala Ile Leu Asn Asn Leu Glu Val Lys Lys Lys Arg Glu
 85 90 95

Pro Phe Thr Asp Thr His Tyr Leu Ser Leu Thr Arg Asp Cys Glu His
 100 105 110

Phe Lys Ala Glu Arg Lys Phe Ile Gln Phe Pro Leu Ser Lys Glu Glu
 115 120 125

Val Glu Phe Pro Ile Ala Tyr Ser Met Val Ile His Glu Lys Ile Glu
 130 135 140

Asn Phe Glu Arg Leu Leu Arg Ala Val Tyr Ala Pro Gln Asn Ile Tyr
 145 150 155 160

Cys Val His Val Asp Glu Lys Ser Pro Glu Thr Phe Lys Glu Ala Val
 165 170 175

Lys Ala Ile Ile Ser Cys Phe Pro Asn Val Phe Ile Ala Ser Lys Leu
180 185 190

Val Arg Val Val Tyr Ala Ser Trp Ser Arg Val Gln Ala Asp Leu Asn
195 200 205

Cys Met Glu Asp Leu Leu Gln Ser Ser Val Pro Trp Lys Tyr Phe Leu
210 215 220

Asn Thr Cys Gly Thr Asp Phe Pro Ile Lys Ser Asn Ala Glu Met Val
225 230 235 240

Gln Ala Leu Lys Met Leu Asn Gly Arg Asn Ser Met Glu Ser Glu Val
245 250 255

Pro Pro Lys His Lys Glu Thr Arg Trp Lys Tyr His Phe Glu Val Val
260 265 270

Arg Asp Thr Leu His Leu Thr Asn Lys Lys Lys Asp Pro Pro Pro Tyr
275 280 285

Asn Leu Thr Met Phe Thr Gly Asn Ala Tyr Ile Val Ala Ser Arg Asp
290 295 300

Phe Val Gln His Val Leu Lys Asn Pro Lys Ser Gln Gln Leu Ile Glu
305 310 315 320

Trp Val Lys Asp Thr Tyr Ser Pro Asp Glu His Leu Trp Ala Thr Leu
325 330 335

Gln Arg Ala Arg Trp Met Pro Gly Ser Val Pro Asn His Pro Lys Tyr
340 345 350

Asp Ile Ser Asp Met Thr Ser Ile Ala Arg Leu Val Lys Trp Gln Gly
355 360 365

His Glu Gly Asp Ile Asp Lys Gly Ala Pro Tyr Ala Pro Cys Ser Gly
370 375 380

Ile His Gln Arg Ala Ile Cys Val Tyr Gly Ala Gly Asp Leu Asn Trp
385 390 395 400

Met Leu Gln Asn His His Leu Leu Ala Asn Lys Phe Asp Pro Lys Val
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Asp Asp Asn Ala Leu Gln Cys Leu Glu Glu Tyr Leu Arg Tyr Lys Ala
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Ile Tyr Gly Thr Glu Leu
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Arg Ile His Gln Lys Pro Glu Phe Val Ser Val Arg His Leu Glu Leu
35 40 45

Ala Gly Glu Asn Pro Ser Ser Asp Ile Asn Cys Thr Lys Val Leu Gln
50 55 60

Gly Asp Val Asn Glu Ile Gln Lys Val Lys Leu Glu Ile Leu Thr Val
65 70 75 80

Lys Phe Lys Lys Arg Pro Arg Trp Thr Pro Asp Asp Tyr Ile Asn Met
85 90 95

Thr Ser Asp Cys Ser Ser Phe Ile Lys Arg Arg Lys Tyr Ile Val Glu
100 105 110

Pro Leu Ser Lys Glu Glu Ala Glu Phe Pro Ile Ala Tyr Ser Ile Val
115 120 125

Val His His Lys Ile Glu Met Leu Asp Arg Leu Leu Arg Ala Ile Tyr
130 135 140

Met Pro Gln Asn Phe Tyr Cys Val His Val Asp Thr Lys Ser Glu Asp
145 150 155 160

Ser Tyr Leu Ala Ala Val Met Gly Ile Ala Ser Cys Phe Ser Asn Val
165 170 175

Phe Val Ala Ser Arg Leu Glu Ser Val Val Tyr Ala Ser Trp Ser Arg
180 185 190

Val Gln Ala Asp Leu Asn Cys Met Lys Asp Leu Tyr Ala Met Ser Ala
195 200 205

Asn Trp Lys Tyr Leu Ile Asn Leu Cys Gly Met Asp Phe Pro Ile Lys
210 215 220

Thr Asn Leu Glu Ile Val Arg Lys Leu Lys Leu Leu Met Gly Glu Asn
225 230 235 240

Asn Leu Glu Thr Glu Arg Met Pro Ser His Lys Glu Glu Arg Trp Lys
245 250 255

Lys Arg Tyr Glu Val Val Asn Gly Lys Leu Thr Asn Thr Gly Thr Val
260 265 270

Lys Met Leu Pro Pro Leu Glu Thr Pro Leu Phe Ser Gly Ser Ala Tyr
275 280 285

Phe Val Val Ser Arg Glu Tyr Val Gly Tyr Val Leu Gln Asn Glu Lys
290 295 300

Ile Gln Lys Leu Met Glu Trp Ala Gln Asp Thr Tyr Ser Pro Asp Glu
305 310 315 320

Tyr Leu Trp Ala Thr Ile Gln Arg Ile Pro Glu Val Pro Gly Ser Leu
325 330 335

Pro Ala Ser His Lys Tyr Asp Leu Ser Asp Met Gln Ala Val Ala Arg
340 345 350

Phe Val Lys Trp Gln Tyr Phe Glu Gly Asp Val Ser Lys Gly Ala Pro
355 360 365

Tyr Pro Pro Cys Asp Gly Val His Val Arg Ser Val Cys Ile Phe Gly
370 375 380

Ala Gly Asp Leu Asn Trp Met Leu Arg Lys His His Leu Phe Ala Asn
385 390 395 400

Lys Phe Asp Val Asp Val Asp Leu Phe Ala Ile Gln Cys Leu Asp Glu
405 410 415

His Leu Arg His Lys Ala Leu Glu Thr Leu Lys His
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Phe Gln Arg Leu Asn Ile Ser Asp Pro Leu Arg Leu Thr Gln Val Cys
35 40 45

Thr Ser Phe Ile Asn Gly Lys Thr Arg Phe Leu Trp Lys Asn Lys Leu
50 55 60

Met Ile His Glu Lys Ser Ser Cys Lys Glu Tyr Leu Thr Gln Ser His
65 70 75 80

Tyr Ile Thr Ala Pro Leu Ser Lys Glu Glu Ala Asp Phe Pro Leu Ala
85 90 95

Tyr Ile Met Val Ile His His His Phe Asp Thr Phe Ala Arg Leu Phe
100 105 110

Arg Ala Ile Tyr Met Pro Gln Asn Ile Tyr Cys Val His Val Asp Glu
115 120 125

Lys Ala Thr Thr Glu Phe Lys Asp Ala Val Glu Gln Leu Leu Ser Cys
130 135 140

Phe Pro Asn Ala Phe Leu Ala Ser Lys Met Glu Pro Val Val Tyr Gly
145 150 155 160

Gly Ile Ser Arg Leu Gln Ala Asp Leu Asn Cys Ile Arg Asp Leu Ser
165 170 175

Ala Phe Glu Val Ser Trp Lys Tyr Val Ile Asn Thr Cys Gly Gln Asp
180 185 190

Phe Pro Leu Lys Thr Asn Lys Glu Leu Val Gln Tyr Leu Lys Gly Phe
195 200 205

Lys Gly Lys Asn Ile Thr Pro Gly Val Leu Pro Pro Ala His Ala Ile
210 215 220

Gly Arg Thr Lys Tyr Val His Gln Glu His Leu Gly Lys Glu Leu Ser
225 230 235 240

Tyr Val Ile Arg Thr Thr Ala Leu Lys Pro Pro Pro Pro His Asn Leu
245 250 255

Thr Ile Tyr Phe Gly Ser Ala Tyr Val Ala Leu Ser Arg Glu Phe Ala
260 265 270

Asn Phe Val Leu His Asp Pro Arg Ala Val Asp Leu Leu Gln Trp Ser
275 280 285

Lys Asp Thr Phe Ser Pro Asp Glu His Phe Trp Val Thr Leu Asn Arg
290 295 300

Ile Pro Gly Val Pro Gly Ser Met Pro Asn Ala Ser Trp Thr Gly Asn
305 310 315 320

Leu Arg Ala Ile Lys Trp Ser Asp Met Glu Asp Arg His Gly Gly Cys
325 330 335

His Gly His Tyr Val His Gly Ile Cys Ile Tyr Gly Asn Gly Asp Leu
340 345 350

Lys Trp Leu Val Asn Ser Pro Ser Leu Phe Ala Asn Lys Phe Glu Leu
355 360 365

Asn Thr Tyr Pro Leu Thr Val Glu Cys Leu Glu Leu Arg His Arg Glu
370 375 380

Arg Thr Leu Asn Gln Ser Glu Thr Ala Ile Gln Pro Ser Trp Tyr Phe
385 390 395 400